



SEQUENCE LISTING

<110> du Pont de Nemours and Company

<120> PLANT DISEASE RESISTANCE GENES

<130> BB1313

<140> 09/857,896

<141>

<150> 60/112,737

<151> 1998-12-18

<160> 42

<170> Microsoft Office 97

<210> 1

<211> 1600

<212> DNA

<213> Oryza sativa

<400> 1

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<210> 2

<211> 290

<212> PRT

<213> Oryza sativa

<400> 2

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<220>
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 <222> (335)
 <223> n = A, C, G, or T

<220>
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<220>
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<220>
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 <222> (493)
 <223> n = A, C, G, or T

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 actattttact tcccagtttg agtttgacat tctcgcggga agaaggagaa gaagttggtg 120
 agcctgtgag aggctgattg cgcggcggcc atggccggag ggggagggaa ggcggcggcg 180
 ggcggcggcg aagcgccggc gataacgctg gagcacacac cgacgtggat cgtctccgcc 240
 gtctgcttcg tcatcgatcat catctcgctg ctcttcgagc gcctgctcca ccgcctgggc 300
 aagaggttga agaagaccgc aagaaccgct ctacnaggga ccctcaagtc aaagaagact 360
 gatgctgctg gggatcatctc gctgctgctg aagtttccag ggctgacgca gaagnagctg 420
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<210> 4
 <211> 81
 <212> PRT
 <213> Oryza sativa

<220>
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 <222> (62)
 <223> Xaa = ANY AMINO ACID

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 20 25 30
 Phe Val Ile Val Ile Ile Ser Leu Leu Phe Glu Arg Leu His Arg
 35 40 45

Leu Gly Lys Arg Leu Lys Lys Thr Ala Arg Thr Ala Leu Xaa Gly Thr
 50 55 60

Leu Lys Ser Lys Lys Thr Asp Ala Ala Gly Val Ile Ser Leu Leu Leu
 65 70 75 80

Lys

<210> 5
 <211> 513
 <212> DNA
 <213> Oryza sativa

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 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (492)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (507)
 <223> n = A, C, G, or T

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 gaactggagg aagacggcga gggagaagaa gaagctccgg gacgccgacg agttcctagc 120
 acagatgagc ggcgacacga cgccgagccg cggctcgtcg ccggtgcacc tgctgcacaa 180
 gcaaagggtg aggtcggaag atccgccgag cgcaccggca tcgccggggt tcgccggaga 240
 ggccagggac atgtaccggg tgcccgtggc gccggtgggt cggccgcgat ggtttaaccg 300
 gatggacccg gataagagga gggcggcgct ctcgtcggcc atccaagttg acatcgccga 360
 ttctgatttc tccttcagtg tacaacggtg atggccgaaa ggtttctctg tacttaaagt 420
 tgtanagcag caaatatagg aagtacaatg tatagttggt acactacata tagaggattt 480
 agaaaagttc antcgatttt tttaagnaac aat 513

<210> 6
 <211> 129
 <212> PRT
 <213> Oryza sativa

<400> 6
 Gln Met Gly Ser Asn Met Lys Lys Thr Ile Phe Glu Glu Gln Thr Met
 1 5 10 15

Lys Ala Leu Met Asn Trp Arg Lys Thr Ala Arg Glu Lys Lys Lys Leu
 20 25 30

Arg Asp Ala Asp Glu Phe Leu Ala Gln Met Ser Gly Asp Thr Thr Pro
 35 40 45

Ser Arg Gly Ser Ser Pro Val His Leu Leu His Lys Gln Arg Val Arg
 50 55 60

Ser Glu Asp Pro Pro Ser Ala Pro Ala Ser Pro Gly Phe Ala Gly Glu

Trp	Val	Val	Ala	Phe	Cys	Thr	Val	Ile	Val	Ala	Ile	Ser	Leu	Ala	
			20				25					30			
Ala	Glu	Arg	Leu	Leu	His	Tyr	Gly	Gly	Lys	Phe	Leu	Lys	Ala	Lys	Asp
		35					40					45			
Gln	Lys	Pro	Leu	Tyr	Glu	Ala	Leu	Gln	Lys	Ile	Lys	Glu	Glu	Leu	Met
	50					55					60				
Leu	Leu	Gly	Phe	Ile	Ser	Leu	Leu	Leu	Thr	Val	Thr	Gln	Asn	Gly	Ile
65					70					75					80
Thr	Lys	Ile	Cys	Val	Arg	Pro	Ser	Leu	Thr	Leu	His	Met	Leu	Pro	Cys
				85					90					95	
Asn	Leu	His	Asp	Ala	Pro	Ala	Asn	His	Glu	Ser	His	Phe	Gln	Thr	Phe
			100					105					110		
Phe	Pro	Gly	Thr	Ala	Arg	Arg	Leu	Leu	Ser	Gly	Glu	His	Ser	Thr	Pro
		115					120					125			
Glu	Ser	Ala	Ser	Lys	Ile	Gly	Tyr	Cys	Ser	Arg	Lys	His	Lys	Val	Pro
	130					135					140				
Leu	Leu	Ser	Val	Glu	Ala	Leu	His	His	Leu	His	Ile	Phe	Ile	Phe	Val
145					150					155					160
Leu	Ala	Val	Val	His	Val	Ser	Phe	Ser	Val	Leu	Thr	Val	Val	Phe	Gly
				165					170					175	
Gly	Ala	Arg	Ile	Arg	Gln	Trp	Lys	His	Trp	Glu	Asp	Ser	Ile	Ala	Lys
			180					185					190		
Gln	Asn	Tyr	Glu	Thr	Asp	Arg	Val	Leu	Lys	Pro	Lys	Val	Thr	Gln	Val
		195					200					205			
His	Gln	His	Asp	Phe	Ile	Arg	Gly	Arg	Phe	Ala	Gly	Phe	Gly	Lys	Asp
	210					215					220				
Ser	Ala	Ile	Val	Gly	Trp	Leu	Leu	Ser	Phe	Leu	Lys	Gln	Phe	Tyr	Gly
225					230					235					240
Ser	Val	Thr	Lys	Ser	Asp	Tyr	Val	Thr	Leu	Arg	His	Gly	Phe	Ile	Met
				245					250					255	
Thr	His	Cys	Arg	Thr	Asn	Pro	Lys	Phe	Asn	Phe	His	Lys	Tyr	Met	Ile
			260					265					270		
Arg	Ala	Leu	Glu	Asp	Asp	Phe	Lys	Gln	Val	Val	Gly	Ile	Ser	Trp	Asp
		275					280					285			
Leu	Trp	Leu	Phe	Val	Val	Ile	Phe	Leu	Leu	Leu	Asn	Ile	Asn	Gly	Trp
	290					295					300				
His	Thr	Tyr	Phe	Trp	Ile	Ala	Phe	Ile	Pro	Val	Ile	Leu	Leu	Leu	Ala
305					310					315					320
Val	Gly	Thr	Lys	Leu	Glu	His	Ile	Ile	Thr	Gln	Leu	Ala	His	Glu	Val
				325					330					335	

Pro Glu Lys His Ala Ala Ile Glu Gly Asp Leu Val Val Gln Pro Ser
 340 345 350
 Asp Glu His Phe Trp Phe His Arg Pro His Val Val Leu Phe Leu Ile
 355 360 365
 His Phe Ile Leu Phe Gln Asn Ala Phe Glu Ile Ala Phe Phe Phe Trp
 370 375 380
 Ile Trp Val Thr Tyr Gly Phe Asp Ser Cys Ile Met Gly Gln Val Arg
 385 390 395 400
 Tyr Ile Val Pro Arg Leu Val Ile Gly Val Phe Ile Gln Val Leu Cys
 405 410 415
 Ser Tyr Ser Thr Leu Pro Leu Tyr Ala Ile Val Thr Gln Met Gly Thr
 420 425 430
 His Tyr Lys Arg Ala Ile Phe Asn Asp His Leu Gln Gln Asn Ile Val
 435 440 445
 Gly Trp Ala Gln Lys Ala Lys Lys Arg Lys Gly Leu Lys Ala Asp Gly
 450 455 460
 Asn Pro Gly Gln Gly Ser Ser Gln Glu Ser Ala Asn Thr Gly Ile Gln
 465 470 475 480
 Leu Gly Ser Ile Phe Lys Lys Ala Thr Ala Pro Gly Asp Ser Ser Ser
 485 490 495
 Ala Pro Lys Ala Asp Gly Ile Ser Ser Val
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<210> 9
 <211> 563
 <212> DNA
 <213> Glycine max

<220>
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 <222> (454)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (504)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (531)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (559)
 <223> n = A, C, G, or T

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tttcgtctgg acagtggcca cgcccggctt gaagaaatgc ttccatatgc acatcgggtc 180
gagcatcatg aaggtcgtgc tggggctggc tcttcagttc ctctgcagct atatcacctt 240
ccccctctac gcgctcgtca cacagatggg atcgaacatg aagaggtcca tcttcgacga 300
gcagacggcc aaggcgctga ccaactggcg gaacacggcc aaggagaaga agaaggtccg 360
agacacggac atgctgatgg cgcagatgat cggcgacgcg acgcccagcc gaggcacgtc 420
gccgatgcct agccgggctt cgtcaccggg gcanctgctt cacaagggca tgggacggtc 480
cgacgattcc cagagcgcg cganctcgcc aaggaccatg gaggaagcta nggacatgta 540
cccggttggtg gtggcgcancc ccg 563

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<210> 10
<211> 187
<212> PRT
<213> Glycine max

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<220>
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<222> (151)
<223> Xaa = ANY AMINO ACID

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<220>
<221> UNSURE
<222> (168)
<223> Xaa = ANY AMINO ACID

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<220>
<221> UNSURE
<222> (177)
<223> Xaa = ANY AMINO ACID

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<220>
<221> UNSURE
<222> (186)
<223> Xaa = ANY AMINO ACID

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<400> 10
Val Ile Lys Gly Ala Pro Val Val Glu Pro Ser Asn Lys Phe Phe Trp
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Phe His Arg Pro Asp Trp Val Leu Phe Phe Ile His Leu Thr Leu Phe
          20             25             30

Gln Asn Ala Phe Gln Met Ala His Phe Val Trp Thr Val Ala Thr Pro
          35             40             45

Gly Leu Lys Lys Cys Phe His Met His Ile Gly Leu Ser Ile Met Lys
 50             55             60

Val Val Leu Gly Leu Ala Leu Gln Phe Leu Cys Ser Tyr Ile Thr Phe
 65             70             75             80

Pro Leu Tyr Ala Leu Val Thr Gln Met Gly Ser Asn Met Lys Arg Ser
          85             90             95

Ile Phe Asp Glu Gln Thr Ala Lys Ala Leu Thr Asn Trp Arg Asn Thr
100             105             110

Ala Lys Glu Lys Lys Lys Val Arg Asp Thr Asp Met Leu Met Ala Gln
115             120             125

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Met Ile Gly Asp Ala Thr Pro Ser Arg Gly Thr Ser Pro Met Pro Ser
 130 135 140

Arg Ala Ser Ser Pro Val Xaa Leu Leu His Lys Gly Met Gly Arg Ser
 145 150 155 160

Asp Asp Ser Gln Ser Ala Pro Xaa Ser Pro Arg Thr Met Glu Glu Ala
 165 170 175

Xaa Asp Met Tyr Pro Val Val Val Ala Xaa Pro
 180 185

<210> 11
 <211> 1938
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (1370)
 <223> n = A, C, G, or T

<400> 11
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 cttttttcttc tttttttccc ccatgtatag ctccaagttc agaaagctgt tttgttctgt 120
 gttgtttttca tggctctgtt ttggaggttt ggccatggca gcagggtgaaa gtagcagcag 180
 ctccagagac ctagaccaga caccaacgtg ggccgttgct gctgtctgta ctgttttcat 240
 cttggtatcc atagcactcg aaaagagtct ccacaaagtt gggacgtggc ttggacaaaa 300
 gaaaaagaag gctttgcttg aaagctctgga gaaggtcaag gctgagttga tgattttagg 360
 tttcattttca ctgcttttga ctttcgggca gagttacatt gtcagaatat gtattcccga 420
 aaagctggca gacaatatgt taccatgtcc gtataaatat aaggaggaca aaaaggcatc 480
 agatagtgaag gaggaacatc gtaggaaact tttatcttat gaacgtagat atttagctgc 540
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 tgggaagccc atttggttaatt cttcaacagt gcactcactg gccccacact acaccgtttc 1620
 aaaactactg gccactcaac ccgctcctca tcaacagcgt acgaggatca agatcaagat 1680
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 attgtaagag ttgatcatgg cgaccaacaa caagcagaac atagacaaga tagtgaggga 1800
 gaaaccaaca gtagtagtga aggtgaattc tcatttgtca aacctgacct tgtggaatt 1860
 agaaccacca catagcatat gatcatatat tcatctctat tcttatacat aaatctttac 1920
 ataaaaaaaa aaaaaaaaa 1938

<210> 12
 <211> 530
 <212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (406)

<223> Xaa = ANY AMINO ACID

<400> 12

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Pro Thr Trp Ala Val Ala Ala Val Cys Thr Val Phe Ile Leu Val Ser
20 25 30

Ile Ala Leu Glu Lys Ser Leu His Lys Val Gly Thr Trp Leu Gly Gln
35 40 45

Lys Lys Lys Lys Ala Leu Leu Glu Ala Leu Glu Lys Val Lys Ala Glu
50 55 60

Leu Met Ile Leu Gly Phe Ile Ser Leu Leu Leu Thr Phe Gly Gln Ser
65 70 75 80

Tyr Ile Val Arg Ile Cys Ile Pro Glu Lys Leu Ala Asp Asn Met Leu
85 90 95

Pro Cys Pro Tyr Lys Tyr Lys Glu Asp Lys Lys Ala Ser Asp Ser Glu
100 105 110

Glu Glu His Arg Arg Lys Leu Leu Ser Tyr Glu Arg Arg Tyr Leu Ala
115 120 125

Ala Asp Thr Thr Ser Phe Lys Cys Ser Arg Glu Gly His Glu Pro Leu
130 135 140

Leu Ser Val Asn Gly Leu His Gln Leu His Ile Leu Arg Ile Leu Leu
145 150 155 160

Ala Val Ile His Val Leu Tyr Ser Ala Ile Thr Met Met Leu Gly Arg
165 170 175

Leu Lys Ile Leu Gly Trp Lys Ala Trp Glu Ala Gly Leu Gln Leu His
180 185 190

Asn Tyr Glu Phe Ala Asn Ala Ala Ser Lys Ile Lys Leu Ile Met Glu
195 200 205

Thr Ser Phe Val Arg Ser Pro Ile Gln Phe Leu Ile Arg Ile Pro Ile
210 215 220

Phe Phe Tyr Ile Arg Cys Phe Phe Arg Gln Phe Tyr Arg Ser Val Asn
225 230 235 240

Arg Thr Asp Tyr Leu Thr Leu Arg Asn Gly Phe Ile Thr Val His Leu
245 250 255

Ala Pro Gly Ser Lys Phe Asn Phe Pro Lys Tyr Ile Lys Arg Ser Leu
260 265 270

Glu Asp Asp Phe Lys Val Val Val Gly Val Ser Pro Ile Leu Trp Ala

275					280					285					
Ser	Val	Val	Val	Tyr	Leu	Leu	Ile	Asn	Val	Asn	Gly	Trp	His	Thr	Val
290					295					300					
Leu	Trp	Ala	Ala	Leu	Ile	Pro	Val	Val	Ile	Ile	Leu	Ala	Val	Gly	Thr
305					310					315					320
Lys	Leu	Gln	Ala	Ile	Leu	Ala	Asn	Met	Ala	Leu	Glu	Ile	Thr	Glu	Arg
				325					330					335	
His	Ala	Val	Val	Gln	Gly	Met	Pro	Leu	Val	Gln	Gly	Ser	Asp	Lys	Tyr
			340					345					350		
Phe	Trp	Phe	Gly	Gln	Pro	Gln	Leu	Val	Leu	His	Leu	Ile	His	Phe	Ala
		355					360					365			
Leu	Phe	Gln	Asn	Ala	Phe	Gln	Ile	Thr	Tyr	Ile	Leu	Trp	Ile	Trp	Tyr
	370					375					380				
Ser	Phe	Gly	Leu	Arg	Asn	Cys	Phe	Arg	Thr	Asp	Tyr	Lys	Leu	Ala	Val
385					390					395					400
Val	Lys	Val	Ala	Leu	Xaa	Met	Met	Leu	Cys	Leu	Cys	Ser	Tyr	Ile	Thr
				405					410					415	
Leu	Pro	Leu	Tyr	Ala	Leu	Val	Thr	Gln	Met	Gly	Ser	Arg	Met	Lys	Thr
			420					425					430		
Ala	Ile	Phe	Asp	Glu	Gln	Thr	Asn	Lys	Ala	Leu	Lys	Lys	Trp	His	Met
		435					440					445			
Ala	Ala	Lys	Lys	Lys	Gln	Gly	Gly	Ala	Val	Thr	Leu	Gly	Lys	Ser	Ser
	450					455					460				
Ala	Arg	Ile	Met	Asp	Gly	Ser	Pro	Ile	Gly	Asn	Ser	Ser	Thr	Val	His
465					470					475				480	
Ser	Leu	Ala	Pro	His	Tyr	Thr	Val	Ser	Lys	Leu	Leu	Ala	Thr	Gln	Pro
				485					490					495	
Ala	Pro	His	Gln	Gln	Arg	Thr	Arg	Ile	Lys	Ile	Lys	Ile	Met	Asn	Met
			500					505					510		
Asn	Pro	Met	Val	Leu	Ser	Cys	Leu	Arg	Trp	Arg	Arg	Lys	Gln	Gln	Ala
	515						520					525			
Ser	Leu														
	530														

<210> 13
 <211> 357
 <212> DNA
 <213> Glycine max

<400> 13
 gcacgagggg atatagagag aggtttagaa gagtgaagag aaaatgggtg gtggaggtga 60
 agaagggaac aatttggaat tcaactccac ttgggttggt gctgttggtt gttctgtgat 120
 tggtgctgct tcgtttgctg ctgaaagggt tcttcattat ggaggggaagt ttctcaagag 180
 gaagaatcag aagccactct atgaagccct ggaaaaaatc aaagaagagt tgatgctggt 240

gggctttatt tctctgctac tgacaataac acaaaatggg atcatcagaa tttgtgttcc 300
 agtgggttgg actcaccata tgcttccttg cagtctaaag gataaaaaaa aaaaaaa 357

<210> 14
 <211> 104
 <212> PRT
 <213> Glycine max

<400> 14
 Met Gly Gly Gly Gly Glu Glu Gly Asn Asn Leu Glu Phe Thr Pro Thr
 1 5 10 15
 Trp Val Val Ala Val Val Cys Ser Val Ile Val Ala Ala Ser Phe Ala
 20 25 30
 Ala Glu Arg Phe Leu His Tyr Gly Gly Lys Phe Leu Lys Arg Lys Asn
 35 40 45
 Gln Lys Pro Leu Tyr Glu Ala Leu Glu Lys Ile Lys Glu Glu Leu Met
 50 55 60
 Leu Leu Gly Phe Ile Ser Leu Leu Leu Thr Ile Thr Gln Asn Gly Ile
 65 70 75 80
 Ile Arg Ile Cys Val Pro Val Gly Trp Thr His His Met Leu Pro Cys
 85 90 95
 Ser Leu Lys Asp Lys Lys Lys Lys
 100

<210> 15
 <211> 678
 <212> DNA
 <213> Triticum aestivum

<400> 15
 gcacgagcgt catcaagggg gcgcccgtgg ttgagcccag caacaagttc ttctggttcc 60
 accgccccga ctgggtcctc ttcttcatac acctgacgct gttccagaat gcgtttcaga 120
 tggcacattt cgtctggaca gtggccacgc ccggcttgaa gaaatgcttc catatgcaca 180
 tcggtctgag catcatgaag gtcgtgctgg ggctggctct tcagttcctc tgcagctata 240
 tcaccttccc cctctacgcg ctcgtcacac agatgggatc gaacatgaag aggtccatct 300
 tcgacgagca gacggccaag gcgctgacca actggcggaa cacggccaag gagaagaaga 360
 aggtccgaga cacggacatg ctgatggcgc agatgatcgg cgacgcgacg cccagccgag 420
 gcacgtcgcc gatgcctagc cgggcttcgt caccggtgca cctgcttcac aagggcagtg 480
 gacggtcoga cgatccccag agcgcgccga cctcgccaag gaccatggag gaggctaggg 540
 acatgtaccc ggttgtggtg gcgcatccc tgcacagact aaatcctgct gacagggcga 600
 ggtcggtctc ttcgtcgga ctcgaggccg acatcccagc gcagattttt ccttcaacca 660
 gggatgagac caagtttt 678

<210> 16
 <211> 221
 <212> PRT
 <213> Triticum aestivum

<400> 16
 Thr Ser Val Ile Lys Gly Ala Pro Val Val Glu Pro Ser Asn Lys Phe
 1 5 10 15
 Phe Trp Phe His Arg Pro Asp Trp Val Leu Phe Phe Ile His Leu Thr
 20 25 30


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gaagcacacg gctattcgag gggatttagt agtttctcct tcagataact tcttttggtt 1080
ccaccggcct aaattagttc ttctgttgat ccacatcggt ctatttcaga atgcatttga 1140
aattgcattt ttcttctggc tcttggtgac atatggtttt aaatcatgca tcatggggaa 1200
accagcatat gttattactc gagttgtcat aagtgtaatc tgccaagtcc tttgtggtta 1260
cagcacccta ccactatacg ccgtcgtctc ccatatgggg aattccttca agaagactat 1320
atttgatgaa aatgtgactg aaggccttgt caactgggct gaaaaggcta ggagaggcac 1380
aagaaccca aataaaatta ctacagatgc aagtagttca ccaattgatg aggcaaagg 1440
tggcgcggtt caaatgacaa atacacgggc aaactcgtcg gtggagcaag gcaacg 1496

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<210> 18
<211> 450
<212> PRT
<213> Triticum aestivum

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<400> 18
Met Ala Gly Gly Gly Gly Lys Ala Lys Pro Leu Glu Tyr Thr Pro Thr
  1           5           10           15

Trp Ile Val Ala Leu Val Cys Ser Val Met Ile Ile Ile Ser Leu Leu
      20           25           30

Phe Glu Arg Leu Leu His Arg Leu Gly Lys Arg Leu Ile Arg Ser Arg
      35           40           45

Lys Lys Pro Leu Tyr Glu Ala Leu Leu Lys Val Lys Glu Glu Leu Met
      50           55           60

Leu Leu Gly Phe Ile Ser Leu Leu Leu Thr Val Phe Gln Gly Pro Met
      65           70           75           80

Gly Lys Val Cys Val Ser Pro Ser Ala Met Leu His Leu Gln Pro Cys
      85           90           95

Ser Arg Arg Arg Thr Arg Arg Thr Thr Ser Ala Thr Pro Cys Ser Pro
      100          105          110

Val Phe His Trp Glu Gly Phe Gly Pro Pro Glu Leu Val Gly Gly Pro
      115          120          125

Ser Ser Ser Asp Glu Tyr Cys Leu Lys Lys Asp Lys Val Pro Leu Leu
      130          135          140

Ser Ser Asp Ala Ile His Gln Leu His Ile Phe Ile Phe Val Leu Ala
      145          150          155          160

Val Thr His Phe Leu Leu Ser Ala Ile Thr Val Leu Leu Gly Met Ala
      165          170          175

Gln Thr Arg Asn Trp Arg His Trp Glu Pro Lys Ile Gln Glu Asn Asn
      180          185          190

Gly Ser Ala Pro Gln Met Ile Lys His Val Gln Glu Phe Lys Phe Ile
      195          200          205

Gln Asp His Phe Lys Gly His Arg Lys Arg Ser Arg Ile Phe Gly Trp
      210          215          220

Met Arg Ser Phe Phe Lys Gln Leu Tyr Gly Ser Val Thr Glu Glu Asp
      225          230          235          240

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Tyr Thr Thr Met Arg Leu Gly Phe Ile Met Lys His Cys Lys Gly Thr
 245 250 255
 Pro Lys Phe Asn Phe Tyr Ser Tyr Met Ile Arg Ala Leu Glu Val Asp
 260 265 270
 Phe Lys Lys Val Val Gly Ile Ser Trp Tyr Leu Trp Ala Met Leu Met
 275 280 285
 Ile Phe Leu Leu Leu Asn Val Glu Gly Trp Tyr Val Tyr Ile Trp Ile
 290 295 300
 Thr Leu Val Pro Phe Ile Met Leu Leu Met Val Gly Ser Lys Met Glu
 305 310 315 320
 His Ile Ile Thr Glu Leu Ala Tyr Glu Val Ala Gln Lys His Thr Ala
 325 330 335
 Ile Arg Gly Asp Leu Val Val Ser Pro Ser Asp Asn Phe Phe Trp Phe
 340 345 350
 His Arg Pro Lys Leu Val Leu Leu Leu Ile His Ile Val Leu Phe Gln
 355 360 365
 Asn Ala Phe Glu Ile Ala Phe Phe Phe Trp Leu Leu Val Thr Tyr Gly
 370 375 380
 Phe Lys Ser Cys Ile Met Gly Lys Pro Ala Tyr Val Ile Thr Arg Val
 385 390 395 400
 Val Ile Ser Val Ile Cys Gln Val Leu Cys Gly Tyr Ser Thr Leu Pro
 405 410 415
 Leu Tyr Ala Val Val Ser His Met Gly Asn Ser Phe Lys Lys Thr Ile
 420 425 430
 Phe Asp Glu Asn Val Thr Glu Gly Leu Val Asn Trp Ala Glu Lys Ala
 435 440 445
 Arg Arg
 450

<210> 19
 <211> 474
 <212> DNA
 <213> Triticum aestivum

<220>
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 <222> (292)
 <223> n = A, C, G, or T

<220>
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 <222> (366)
 <223> n = A, C, G, or T

<220>
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 <222> (372)

<223> n = A, C, G, or T

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<222> (383)

<223> n = A, C, G, or T

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<222> (410)

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<222> (418)

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<222> (428)

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<222> (441)

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<221> unsure

<222> (454)

<223> n = A, C, G, or T

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<221> unsure

<222> (468)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (474)

<223> n = A, C, G, or T

<400> 19

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caccacatg ggcggcgaca tcaagctgca ggcgttcggc gagcacgtac acgtgtccgt 180
gcacagctgg gcgacggacg tgaagaagaa ggcgacgtcg ctgccggccc atccgcaccc 240
gcaccagcac ccgcaactcg aactccggat tccgtttctc aacaatgaag cngcacagcg 300
gaccttgacc ttgcaaccga ggaagctgca gccgcggcga agggcgacgg agcaacgcgc 360
tggaantcca antctccac cgnaccgccg gaacaacggg ccgacactan aggaattngt 420
gacacaangg gggagacatc ntctcgaacg ccanttcctt acggctanat cccn 474
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<210> 20

<211> 133

<212> PRT

<213> *Triticum aestivum*

<220>

<221> UNSURE

<222> (122)

<223> Xaa = ANY AMINO ACID

<220>

<221> UNSURE

<222> (124)

<223> Xaa = ANY AMINO ACID

<220>

<221> UNSURE

<222> (128)

<223> Xaa = ANY AMINO ACID

<400> 20

Thr Tyr Gly Phe Asp Ser Cys Ile Met Glu Asn Arg Ser Tyr Ala Ile
1 5 10 15

Pro Arg Leu Ala Ile Gly Ile Ile Val Gln Val Leu Cys Ser Tyr Ser
20 25 30

Thr Leu Pro Leu Tyr Ala Ile Val Thr His Met Gly Gly Asp Ile Lys
35 40 45

Leu Gln Ala Phe Gly Glu His Val His Val Ser Val His Ser Trp Ala
50 55 60

Thr Asp Val Lys Lys Lys Ala Thr Ser Leu Pro Ala His Pro His Pro
65 70 75 80

His Gln His Pro His Ser Gln Leu Arg Ile Pro Phe Leu Asn Asn Glu
85 90 95

Ala Ala Gln Arg Thr Leu Thr Leu Gln Pro Arg Lys Leu Gln Pro Arg
100 105 110

Arg Arg Ala Thr Glu Gln Arg Ala Gly Xaa Pro Xaa Leu Pro Pro Xaa
115 120 125

Arg Arg Asn Asn Gly
130

<210> 21

<211> 548

<212> DNA

<213> Oryza sativa

<220>

<221> unsure

<222> (516)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (526)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (545)

<223> n = A, C, G, or T

<400> 21
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 gaagcagatt ttaagaaagt gggttggtata agctgggtact tgtggatatt cgttatgata 120
 ttcctgctgc tgaatgttaa tggttggcac acatactttt ggatctcctt cgttcccctt 180
 ctacttttgc tggccgttgg caccaagcta gaacatgtca taaccaact agcccatgag 240
 gttgccgaga agcactctgc aattgagggc gacttggttg tgaatccatc agacgagcac 300
 ttttggtttg gacggccgaa ggtgataccta tacctgatcc attttatact cttccaaaac 360
 gcgttcgaga tcgcgttctt cttctggatt ctgaccacct acggtttcaa ctctgcgcatc 420
 aagggaccaa cgtccctttt atcctgacaa ggcttatcat cgggggcatc gttcaaatacc 480
 tctgcaacta caagtacctt gcctaataata tgcaantgtc acacanatgg ggctcccttt 540
 ttaanaaa 548

<210> 22
 <211> 156
 <212> PRT
 <213> Oryza sativa

<400> 22
 Tyr Arg Tyr Met Val Arg Ala Leu Glu Ala Asp Phe Lys Lys Val Val
 1 5 10 15
 Gly Ile Ser Trp Tyr Leu Trp Ile Phe Val Met Ile Phe Leu Leu Leu
 20 25 30
 Asn Val Asn Gly Trp His Thr Tyr Phe Trp Ile Ser Phe Val Pro Leu
 35 40 45
 Leu Leu Leu Leu Ala Val Gly Thr Lys Leu Glu His Val Ile Thr Gln
 50 55 60
 Leu Ala His Glu Val Ala Glu Lys His Ser Ala Ile Glu Gly Asp Leu
 65 70 75 80
 Val Val Asn Pro Ser Asp Glu His Phe Trp Phe Gly Arg Pro Lys Val
 85 90 95
 Ile Leu Tyr Leu Ile His Phe Ile Leu Phe Gln Asn Ala Phe Glu Ile
 100 105 110
 Ala Phe Phe Phe Trp Ile Leu Thr Thr Tyr Gly Phe Asn Ser Cys Ile
 115 120 125
 Lys Gly Thr Asn Val Pro Phe Ile Leu Thr Arg Leu Ile Ile Gly Gly
 130 135 140
 Ile Val Gln Ile Leu Cys Asn Tyr Lys Tyr Leu Ala
 145 150 155

<210> 23
 <211> 738
 <212> DNA
 <213> Oryza sativa

<220>
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 <222> (459)
 <223> n = A, C, G, or T

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<221> unsure
<222> (600)
<223> n = A, C, G, or T

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<222> (606) .. (607)
<223> n = A, C, G, or T

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<222> (658)
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<222> (661)
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<222> (672)
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<222> (675)
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<222> (679)
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<222> (683)
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<222> (696)
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<220>
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<222> (707)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (721)
<223> n = A, C, G, or T

<400> 23
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aagctggagc tcataagcac taggctggca caagaggcag cagactgccc agatgaagca 120
acaggaaacc cctggacaaa gccatgcaag gagcacttct gggttcagcaa gcctaggatt 180
gtcctccatt tgatccactt catcctgttc cagaactcct ttgagatggg ttttttcttc 240
tgggttcttg caacatatgg gtttgattca tgcacatggg agaacaagat ttatgccctc 300

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cccagacttg ctattggaat catcgtccag gtgctctgca gctacagcac gctgccgcta 360
tacgccatcg ttaccacat gggcgggggac atcaagctgc aggcgttcgg cgagacggtg 420
cacgtgtcgg tgcacagctg ggcgacggac gtgaggaana agaaggcggc gccgccgccc 480
cactcccacc tccgcatccc cttcctcatg aagcgacgcc acagcaccgc cggcgccgac 540
gacgccgcgg acgacgcggc cggcgacgtc gaccaccaac accaccatca cgggcaccan 600
catcanngtc accaacaaca acgaggggag ctccgtcggg ggcggggcggg ggccggtnct 660
nggagggaga tngtngccna acnacgtcct ggcggncgag gacgggncac ccggccgggc 720
nccgccgcct tttttttt 738

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<210> 24
<211> 155
<212> PRT
<213> Oryza sativa

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<220>
<221> UNSURE
<222> (153)
<223> Xaa = ANY AMINO ACID

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<400> 24
Leu Thr Thr Tyr Phe Trp Leu Ser Phe Leu Pro Leu Ile Leu Leu Leu
 1             5             10             15

Ile Val Gly Thr Lys Leu Glu Leu Ile Ser Thr Arg Leu Ala Gln Glu
          20             25             30

Ala Ala Asp Cys Pro Asp Glu Ala Thr Gly Asn Pro Trp Thr Lys Pro
 35             40             45

Cys Lys Glu His Phe Trp Phe Ser Lys Pro Arg Ile Val Leu His Leu
 50             55             60

Ile His Phe Ile Leu Phe Gln Asn Ser Phe Glu Met Gly Phe Phe Phe
 65             70             75             80

Trp Val Leu Ala Thr Tyr Gly Phe Asp Ser Cys Ile Met Glu Asn Lys
          85             90             95

Ile Tyr Ala Leu Pro Arg Leu Ala Ile Gly Ile Ile Val Gln Val Leu
 100            105            110

Cys Ser Tyr Ser Thr Leu Pro Leu Tyr Ala Ile Val Thr His Met Gly
 115            120            125

Gly Asp Ile Lys Leu Gln Ala Phe Gly Glu Thr Val His Val Ser Val
 130            135            140

His Ser Trp Ala Thr Asp Val Arg Xaa Lys Lys
145            150            155

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<210> 25
<211> 574
<212> DNA
<213> Oryza sativa

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<220>
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<222> (17)
<223> n = A, C, G, or T

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<220>
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 <222> (353)
 <223> n = A, C, G, or T

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 <222> (437)
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 <222> (455)
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<220>
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 <222> (536)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (555)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (557)
 <223> n = A, C, G, or T

<400> 25
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 ttcccttctg cttagecgtct tccaaaaatt tatcaatcac atttgcatcc cggagagtgc 120
 tgcacatctc atgcttccat gcattactag agagacgtcc gagaccacag aagatgcttc 180
 caaactttgc aagcgaaagg gtgaagttcc tatgctatct gaagaggctt tgcacagct 240
 gcacatcttt atctttgtcc ttggtattgt ccatgttgta ttttgtgta caacattggt 300
 acttggtgga gccaaagatga aaaaatggga agaaatggga gaaagaaatt cancaaggaa 360
 gaaccaagga gcgaccaaag aggccaggct ggatgaaatt cattgttgta agatgtgcca 420
 tctcattctt gaagcanttt tatgattctg ttggnaaacc tggattatca agtacttaag 480
 atcagctttt ggtcaagagg gcactaccaa accgtcctgg attttgattt ccacangtac 540
 aagggtccg tgccnctga gcatgacttt taag 574

<210> 26
 <211> 111
 <212> PRT
 <213> Oryza sativa

<220>
 <221> UNSURE
 <222> (6)
 <223> Xaa = ANY AMINO ACID

<400> 26
 Cys Leu Pro Tyr Asp Xaa Pro Asp Tyr Ala His Met Ala Met Glu Ala
 1 5 10 15
 Ser Gly Phe Ile Ser Phe Leu Leu Ser Val Phe Gln Lys Phe Ile Asn
 20 25 30
 His Ile Cys Ile Pro Glu Ser Ala Ala His Leu Met Leu Pro Cys Ile

35 40 45
 Thr Arg Glu Thr Ser Glu Thr Thr Glu Asp Ala Ser Lys Leu Cys Lys
 50 55 60
 Arg Lys Gly Glu Val Pro Met Leu Ser Glu Glu Ala Leu His Gln Leu
 65 70 75 80
 His Ile Phe Ile Phe Val Leu Gly Ile Val His Val Val Phe Cys Val
 85 90 95
 Thr Thr Leu Leu Leu Gly Gly Ala Lys Met Lys Lys Trp Glu Glu
 100 105 110

<210> 27
 <211> 960
 <212> DNA
 <213> Glycine max

<400> 27
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 ggaaacacct acatgggctg tggccgttgt ttgcttcgtt ttgctctcca tatctatctt 120
 gatcgagcac atcctgcac tcattggaaa gtggttgaag aagaagcaca agagagctct 180
 atgcgaggca ctgaaaaaga tcaaatacaga gcttatgcta ttggggttca tatcggttgc 240
 cctaacggta ggacaaggct taatatcgag gatatgtata tcagaaaagg ttgcggggac 300
 atttcacccc tgtccaaaaa aatactataa gaagaaggaa gagtcagagc accgaaccaa 360
 taatggtcgg agattactag cggcttttct cgattccgat aacccaaatc accgtcgtat 420
 tttggcggcg ggaggtggtg acaactgtcc cccgggtaaa gtcccgtttg tctcatccga 480
 ggggtattcat caactccata ttttatctt cgtgctggct gtctttcatg tcctttactg 540
 catactcact ctagctctgg gtagagcaaa gatgagaagg tggaaacgat gggaagagga 600
 aaccaagaca gcacagtacc aattttcaca cgatcctgaa cgatttagat ttgcgagaga 660
 aacatcattt gggagaagac acctgagttt ctgggcccaa aatcctgtcc tcctctggat 720
 tgtttgtttc ttcaggcagt ttgtacggct agttcctaaa gtggattact tgacactgag 780
 gcatggattt atgatggcac atttggggcc tcatagtcac ccgaaattcg actttcggca 840
 atatatcaaa agatcttttg aagaggactt caaagtggct gttgaaatca ggtttttcgc 900
 ttaattcggg ccatctatgt cttttagggt ttcttttggt acaaaaaaaaaa aaaaaaaaaa 960

<210> 28
 <211> 287
 <212> PRT
 <213> Glycine max

<400> 28
 Met Gly Gly Lys Thr Leu Gln Glu Thr Pro Thr Trp Ala Val Ala Val
 1 5 10 15
 Val Cys Phe Val Leu Leu Ser Ile Ser Ile Leu Ile Glu His Ile Leu
 20 25 30
 His Leu Ile Gly Lys Trp Leu Lys Lys Lys His Lys Arg Ala Leu Cys
 35 40 45
 Glu Ala Leu Glu Lys Ile Lys Ser Glu Leu Met Leu Leu Gly Phe Ile
 50 55 60
 Ser Leu Leu Leu Thr Val Gly Gln Gly Leu Ile Ser Arg Ile Cys Ile
 65 70 75 80
 Ser Glu Lys Val Ala Gly Thr Phe His Pro Cys Pro Lys Lys Tyr Tyr
 85 90 95

Lys Lys Lys Glu Glu Ser Glu His Arg Thr Asn Asn Gly Arg Arg Leu
 100 105 110
 Leu Ala Ala Phe Leu Asp Ser Asp Asn Gln Asn His Arg Arg Ile Leu
 115 120 125
 Ala Ala Gly Gly Gly Asp Asn Cys Pro Pro Gly Lys Val Pro Phe Val
 130 135 140
 Ser Ser Glu Gly Ile His Gln Leu His Ile Phe Ile Phe Val Leu Ala
 145 150 155 160
 Val Phe His Val Leu Tyr Cys Ile Leu Thr Leu Ala Leu Gly Arg Ala
 165 170 175
 Lys Met Arg Arg Trp Lys Arg Trp Glu Glu Glu Thr Lys Thr Ala Gln
 180 185 190
 Tyr Gln Phe Ser His Asp Pro Glu Arg Phe Arg Phe Ala Arg Glu Thr
 195 200 205
 Ser Phe Gly Arg Arg His Leu Ser Phe Trp Ala Gln Asn Pro Val Leu
 210 215 220
 Leu Trp Ile Val Cys Phe Phe Arg Gln Phe Val Arg Ser Val Pro Lys
 225 230 235 240
 Val Asp Tyr Leu Thr Leu Arg His Gly Phe Met Met Ala His Leu Gly
 245 250 255
 Pro His Ser His Pro Lys Phe Asp Phe Arg Gln Tyr Ile Lys Arg Ser
 260 265 270
 Leu Glu Glu Asp Phe Lys Val Val Val Glu Ile Arg Phe Phe Ala
 275 280 285

<210> 29
 <211> 476
 <212> DNA
 <213> Glycine max

<220>
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 <222> (223)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (248)..(249)
 <223> n = A, C, G, or T

<220>
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 <222> (254)
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<220>
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<221> unsure

<222> (330)

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<221> unsure

<222> (341)

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<221> unsure

<222> (350)

<223> n = A, C, G, or T

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<221> unsure

<222> (361)

<223> n = A, C, G, or T

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<221> unsure

<222> (389)

<223> n = A, C, G, or T

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<221> unsure

<222> (405)

<223> n = A, C, G, or T

<220>

<221> unsure

<222> (446)

<223> n = A, C, G, or T

<400> 29

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ctacttcaaa tacaccattc tcaagcaggc caggaacccc gacacatggc atgtctccag 180
ttcacttgct tcacaagcac cctagacaca gtgacagtcc aantatttct cccaagggca 240
tacaattnnc aaanatgaac aatgggggtt ttaaagggat acattccccc caggcaacaa 300
cgcaaggaat naatgttctt attaatgaan agaccatgca nattcaaatn caagattcaa 360
naacaacggg caacttcaac agcaagatnc ctctaattgg gaccnatccc tatccgaatc 420
aacaatgaat ccacattctt aacctnaatt cattttggaa ggggacacac acttgt 476
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<210> 30

<211> 77

<212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (74)

<223> Xaa = ANY AMINO ACID

<400> 30

Ala Leu Val Thr Gln Met Gly Ser Thr Met Lys Val Thr Ile Phe Asn

1

5

10

15

Glu Asn Val Ala Val Ala Leu Lys Asn Trp His His Thr Ala Lys Lys
 20 25 30

His Ile Lys His Asn Lys Asp Ser Thr Ser Asn Thr Pro Phe Ser Ser
 35 40 45

Arg Pro Gly Thr Pro Thr His Gly Met Ser Pro Val His Leu Leu His
 50 55 60

Lys His Pro Arg His Ser Asp Ser Pro Xaa Ile Ser Pro
 65 70 75

<210> 31
 <211> 1711
 <212> DNA
 <213> Triticum aestivum

<400> 31
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 gtggcgctcg tcttcgccgt catgatcatc gtgtccgtcc tcctggagca cgcgctccac 120
 aagctcggcc attggttcca caagcggcac aagaacgcgc tggcggaggc gctggagaag 180
 atcaaagcgg agctgatgct ggtgggggttc atctcgctgc tgctcgccgt gacgcaggac 240
 ccaatctccg ggatatgcat ctccgagaag gccgccagca tcatgcggcc ctgcagcctg 300
 ccccttggtt ccgtcaagag caagtacaaa gactactact gcgccaaaaa gggcaagggtg 360
 tcgctaattgt ccacgggcag cttgcaccag ctccacatat tcatcttcgt gctcgccgtc 420
 ttccatgtca cctacagcgt catcatcatg gctctaagcc gtctcaaaat gaggacatgg 480
 aagaaatggg agacagagac cgcctccttg gaataccagt tcgcaaata tcttgcgcgg 540
 ttccgcttca cgcaccagac gtcgttcgtg aagcggcacc tgggcctctc cagcaccccc 600
 ggcacatgat ggggtggtggc cttcttcagg cagtcttcca ggtcggtcac caaggtggac 660
 tacctcacc tgagggcagg cttcatcaac gcgcatttgt cgcataacag caagtctcag 720
 ttccacaagt acatcaagag gtccatggag gacgacttca aagtcgtcgt tggcatcagc 780
 ctcccgtgt ggtgtgtggc gatcctcacc ctcttccttg atattgacgg gatcggcacg 840
 ctcacctgga tttctttcat cctctcgtc atcctcttgt gtgttggaac caagctggag 900
 atgatcatca tggagatggc cctggagatc caggaccggg cgagcgtcat caagggggcg 960
 cccgtgggtg agcccagcaa caagttcttc tggttccacc gcccgcactg ggtcctcttc 1020
 ttcatacacc tgacgctgtt ccagaatgcg ttccagatgg cacatttcgt ctggacagtg 1080
 gccacgccc gcttgaagaa atgcttccat atgcacatcg gtctgagcat catgaaggtc 1140
 gtgtcggggc tggctcttca gttcctctgc agctatatca ccttccccct ctacgcgctc 1200
 gtcacacaga tgggatcgaa catgaagagg tccatcttcg acgagcagac ggccaaggcg 1260
 ctgaccaact ggcggaacac ggccaaggag aagaagaagg tccgagacac ggacatgctg 1320
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 gatgccgaca tccccagcgc agatttttcc ttcagccagg gatgagacaa gtttatgtat 1620
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<210> 32
 <211> 534
 <212> PRT
 <213> Triticum aestivum

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 Pro Ser Trp Ala Val Ala Leu Val Phe Ala Val Met Ile Ile Val Ser
 20 25 30

Val	Leu	Leu	Glu	His	Ala	Leu	His	Lys	Leu	Gly	His	Trp	Phe	His	Lys	35	40	45
Arg	His	Lys	Asn	Ala	Leu	Ala	Glu	Ala	Leu	Glu	Lys	Ile	Lys	Ala	Glu	50	55	60
Leu	Met	Leu	Val	Gly	Phe	Ile	Ser	Leu	Leu	Leu	Ala	Val	Thr	Gln	Asp	65	70	75
Pro	Ile	Ser	Gly	Ile	Cys	Ile	Ser	Glu	Lys	Ala	Ala	Ser	Ile	Met	Arg	85	90	95
Pro	Cys	Ser	Leu	Pro	Pro	Gly	Ser	Val	Lys	Ser	Lys	Tyr	Lys	Asp	Tyr	100	105	110
Tyr	Cys	Ala	Lys	Lys	Gly	Lys	Val	Ser	Leu	Met	Ser	Thr	Gly	Ser	Leu	115	120	125
His	Gln	Leu	His	Ile	Phe	Ile	Phe	Val	Leu	Ala	Val	Phe	His	Val	Thr	130	135	140
Tyr	Ser	Val	Ile	Ile	Met	Ala	Leu	Ser	Arg	Leu	Lys	Met	Arg	Thr	Trp	145	150	155
Lys	Lys	Trp	Glu	Thr	Glu	Thr	Ala	Ser	Leu	Glu	Tyr	Gln	Phe	Ala	Asn	165	170	175
Asp	Pro	Ala	Arg	Phe	Arg	Phe	Thr	His	Gln	Thr	Ser	Phe	Val	Lys	Arg	180	185	190
His	Leu	Gly	Leu	Ser	Ser	Thr	Pro	Gly	Ile	Arg	Trp	Val	Val	Ala	Phe	195	200	205
Phe	Arg	Gln	Phe	Phe	Arg	Ser	Val	Thr	Lys	Val	Asp	Tyr	Leu	Thr	Leu	210	215	220
Arg	Ala	Gly	Phe	Ile	Asn	Ala	His	Leu	Ser	His	Asn	Ser	Lys	Phe	Asp	225	230	235
Phe	His	Lys	Tyr	Ile	Lys	Arg	Ser	Met	Glu	Asp	Asp	Phe	Lys	Val	Val	245	250	255
Val	Gly	Ile	Ser	Leu	Pro	Leu	Trp	Cys	Val	Ala	Ile	Leu	Thr	Leu	Phe	260	265	270
Leu	Asp	Ile	Asp	Gly	Ile	Gly	Thr	Leu	Thr	Trp	Ile	Ser	Phe	Ile	Pro	275	280	285
Leu	Val	Ile	Leu	Leu	Cys	Val	Gly	Thr	Lys	Leu	Glu	Met	Ile	Ile	Met	290	295	300
Glu	Met	Ala	Leu	Glu	Ile	Gln	Asp	Arg	Ala	Ser	Val	Ile	Lys	Gly	Ala	305	310	315
Pro	Val	Val	Glu	Pro	Ser	Asn	Lys	Phe	Phe	Trp	Phe	His	Arg	Pro	Asp	325	330	335
Trp	Val	Leu	Phe	Phe	Ile	His	Leu	Thr	Leu	Phe	Gln	Asn	Ala	Phe	Gln	340	345	350

Met Ala His Phe Val Trp Thr Val Ala Thr Pro Gly Leu Lys Lys Cys
 355 360 365

 Phe His Met His Ile Gly Leu Ser Ile Met Lys Val Val Leu Gly Leu
 370 375 380

 Ala Leu Gln Phe Leu Cys Ser Tyr Ile Thr Phe Pro Leu Tyr Ala Leu
 385 390 395 400

 Val Thr Gln Met Gly Ser Asn Met Lys Arg Ser Ile Phe Asp Glu Gln
 405 410 415

 Thr Ala Lys Ala Leu Thr Asn Trp Arg Asn Thr Ala Lys Glu Lys Lys
 420 425 430

 Lys Val Arg Asp Thr Asp Met Leu Met Ala Gln Met Ile Gly Asp Ala
 435 440 445

 Thr Pro Ser Arg Gly Thr Ser Pro Met Pro Ser Arg Ala Ser Ser Pro
 450 455 460

 Val His Leu Leu His Lys Gly Met Gly Arg Ser Asp Asp Pro Gln Ser
 465 470 475 480

 Ala Pro Thr Ser Pro Arg Thr Met Glu Glu Ala Arg Asp Met Tyr Pro
 485 490 495

 Val Val Val Ala His Pro Val His Arg Leu Asn Pro Ala Asp Arg Arg
 500 505 510

 Arg Ser Val Ser Ser Ser Ala Leu Asp Ala Asp Ile Pro Ser Ala Asp
 515 520 525

 Phe Ser Phe Ser Gln Gly
 530

<210> 33
 <211> 482
 <212> DNA
 <213> Triticum aestivum

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<220>
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 <222> (177)
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<400> 33

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ctgctccggc acggcactta natagctcct tcgtccaaac gaaacgactg gtacgggtgct 120
tgtgcgtgtg tctcgttgat cgatcgaggt ggtcgtttgc tcggcaccta aaaagangtt 180
gagcggcggg tcatggcggg gccggcggga gggcgggaac tgccggacac cccgacgtgg 240
gcgggtgggg tcgtctgcgc cgttatgata ctcgtctccn tcgccatggg gcacgccctc 300
cacaacctcg ggcactgggt ccacaagcgg cacaanaang gcatngcggg ggcgctggag 360
aaaattaagg nggggctcan gcttggtggg gcttcatanc cctgntcctc anccgtgggg 420
caggaacca tntccaagat atgcaatctc cntggagggg cngcancaaa gaatgntccc 480
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<210> 34

<211> 66

<212> PRT

<213> *Triticum aestivum*

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<220>

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<223> Xaa = ANY AMINO ACID

<220>

<221> UNSURE

<222> (63)

<223> Xaa = ANY AMINO ACID

<400> 34

Met Ala Gly Pro Ala Gly Gly Arg Glu Leu Pro Asp Thr Pro Thr Trp

1	5	10	15
Ala Val Gly Leu Val Cys Ala Val Met Ile Leu Val Ser Xaa Ala Met			
20	25	30	
Gly His Ala Leu His Asn Leu Gly His Trp Phe His Lys Arg His Xaa			
35	40	45	
Xaa Gly Xaa Ala Xaa Ala Leu Glu Lys Ile Lys Xaa Gly Leu Xaa Leu			
50	55	60	
Gly Gly			
65			

<210> 35
 <211> 462
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (19)
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<220>
 <221> unsure
 <222> (328)
 <223> n = A, C, G, or T

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 <222> (382)
 <223> n = A, C, G, or T

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 <222> (394)
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<220>
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 cgtgaaaaga ggccaggctg gatgaaacca tctgctgtaa gatggattat tgcattcttc 120
 aagcagtttt ataattctgt cggtaaacca gattatcaag tactcagatc agcttttggt 180
 ctgcggcact acccaaatcg ccagactttt gatttccaca agtacatggt tcgtgccttg 240
 aagcatgatt tcaaagaagt agttggaatc agctgggtacc tatggctttt cgttatcgtc 300
 ttctctgctgc tgaatataaa tgggtggnac acatacttct ggctgtcttt cttgcccttg 360
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 aagaaagcaa cggatttggt ctggatgaaa gcnatcaagg ga 462

<210> 36
 <211> 127
 <212> PRT
 <213> Triticum aestivum

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 <222> (7)
 <223> Xaa = ANY AMINO ACID

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 <222> (110)
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<400> 36
 Ala Lys Met Arg Thr Trp Xaa Lys Trp Glu Lys Glu Ile Gln Gln Gly
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 Arg Leu Asn Glu Arg Glu Lys Arg Pro Gly Trp Met Lys Pro Ser Ala
 20 25 30
 Val Arg Trp Ile Ile Ala Phe Phe Lys Gln Phe Tyr Asn Ser Val Gly
 35 40 45
 Lys Pro Asp Tyr Gln Val Leu Arg Ser Ala Phe Val Leu Arg His Tyr
 50 55 60
 Pro Asn Arg Pro Asp Phe Asp Phe His Lys Tyr Met Val Arg Ala Leu
 65 70 75 80
 Lys His Asp Phe Lys Glu Val Val Gly Ile Ser Trp Tyr Leu Trp Leu
 85 90 95
 Phe Val Ile Val Phe Leu Leu Leu Asn Ile Asn Gly Trp Xaa Thr Tyr
 100 105 110
 Phe Trp Leu Ser Phe Leu Pro Leu Ile Pro Leu Leu Ile Val Gly
 115 120 125

<210> 37
 <211> 1666
 <212> DNA
 <213> Triticum aestivum

<400> 37
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 cttcgagcgc ttgctccacc gcctaggcaa gaggtgata aggagccgta agaagccgct 180
 gtacgaggcc ctcttgaagg tgaaggagga gctgatgctg ctgggggttca tctcgctgct 240
 gctcacggtg ttccagggtc ccatggggaa ggtgtgctgc agcccgagcg ccatgctcca 300
 cctgcagccc tgcaagccgc cgccgcacga gacggaccac ctcggcgacg ccgtgttcac 360
 cggcggtgctg ggtggggcga ggcgcctcct ggctggagga gctcctcct cgcacaaata 420
 ctgcctcaag aaggacaaag ttccattact ttcatctgac gctattcatc aattgcacat 480
 atttatcttt gtgttggcgg tcacccattt ccttctcagt gctattacag ttcttctagg 540
 aatggcacag acgagaaatt ggcgacattg ggagaccaag atccaagaaa ataatggcag 600
 tgcacctcaa atgatcaagc atgttcaaga attcaaattt attcaagacc acttcaaagg 660
 tcatagaaaa cggtcgagga tatttgggtg gatgcgttcc ttcttcaaac aattgtatgg 720
 atcggtcacc gaggaggact acacaacaat gagacttggg ttcatcatga aacactgtaa 780
 ggaacacca aaattcaact tttatagtta catgatcagg gctttggagg ttgactttaa 840
 gaaagtogtt ggtattagtt ggtacctttg ggccatgttg atgatattcc tactattgaa 900
 tggtgaaggg tggatgtct acatttggat caccttgggt ccattcatta tgttacttat 960
 ggtaggaagt aagatggagc acatcataac ggaattggct tatgaggttg cccagaagca 1020
 cacggctatt cgaggggatt tagtagtttc tccttcagat aacttctttt gggtccaccg 1080
 gcctaaatta gttcttctgt tgatccacat cgtgctatth cagaatgcat ttgaaattgc 1140
 atttttcttc tggctcttgg tgacatatgg ttttaaata tgcacatggg ggaaaccagc 1200

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atatgttatt actcgagttg tcataagtgt aatctgccaa gtcctttgtg gttacagcac 1260
cctaccacta tacgccgtcg tctcccatat ggggaattcc ttcaagaaga ctatatattga 1320
tgaaaatgtg actgaaggcc ttgtcaactg ggctgaaaag gctaggagag gcacaagaac 1380
cccaaataaa attactacag atgcaagtag ttcaccaatt gatgaggcaa atggtggcgc 1440
ggttcaaatg acaaatacac gggcaaactc gtcggtggag caaggcaccg ctaggttgat 1500
ataatcatgt acattagttg ctaatacaaa ggttccatgg gcaacaattt tggcaagtgg 1560
acagatttat tttttgaggg catcacatat ctttaataat gcacgggaat catgtgttcc 1620
cgttttttaa ccaaaaagag aaataacccc cctctaaaaa gaaaca 1666

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<210> 38
<211> 492
<212> PRT
<213> Triticum aestivum

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<400> 38
Met Ala Gly Gly Gly Gly Lys Ala Lys Pro Leu Glu Tyr Thr Pro Thr
  1                      5                      10                      15

Trp Ile Val Ala Leu Val Cys Ser Val Met Ile Ile Ile Ser Leu Leu
      20                      25                      30

Phe Glu Arg Leu Leu His Arg Leu Gly Lys Arg Leu Ile Arg Ser Arg
      35                      40                      45

Lys Lys Pro Leu Tyr Glu Ala Leu Leu Lys Val Lys Glu Glu Leu Met
      50                      55                      60

Leu Leu Gly Phe Ile Ser Leu Leu Leu Thr Val Phe Gln Gly Pro Met
      65                      70                      75                      80

Gly Lys Val Cys Val Ser Pro Ser Ala Met Leu His Leu Gln Pro Cys
      85                      90                      95

Lys Pro Pro Pro His Glu Thr Asp His Leu Gly Asp Ala Val Phe Thr
      100                     105                     110

Gly Val Leu Gly Gly Ala Arg Arg Leu Leu Ala Gly Gly Ala Ser Ser
      115                     120                     125

Ser Asp Lys Tyr Cys Leu Lys Lys Asp Lys Val Pro Leu Leu Ser Ser
      130                     135                     140

Asp Ala Ile His Gln Leu His Ile Phe Ile Phe Val Leu Ala Val Thr
      145                     150                     155                     160

His Phe Leu Leu Ser Ala Ile Thr Val Leu Leu Gly Met Ala Gln Thr
      165                     170                     175

Arg Asn Trp Arg His Trp Glu Thr Lys Ile Gln Glu Asn Asn Gly Ser
      180                     185                     190

Ala Pro Gln Met Ile Lys His Val Gln Glu Phe Lys Phe Ile Gln Asp
      195                     200                     205

His Phe Lys Gly His Arg Lys Arg Ser Arg Ile Phe Gly Trp Met Arg
      210                     215                     220

Ser Phe Phe Lys Gln Leu Tyr Gly Ser Val Thr Glu Glu Asp Tyr Thr
      225                     230                     235                     240

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Thr Met Arg Leu Gly Phe Ile Met Lys His Cys Lys Gly Thr Pro Lys
 245 250 255
 Phe Asn Phe Tyr Ser Tyr Met Ile Arg Ala Leu Glu Val Asp Phe Lys
 260 265 270
 Lys Val Val Gly Ile Ser Trp Tyr Leu Trp Ala Met Leu Met Ile Phe
 275 280 285
 Leu Leu Leu Asn Val Glu Gly Trp Tyr Val Tyr Ile Trp Ile Thr Leu
 290 295 300
 Val Pro Phe Ile Met Leu Leu Met Val Gly Ser Lys Met Glu His Ile
 305 310 315 320
 Ile Thr Glu Leu Ala Tyr Glu Val Ala Gln Lys His Thr Ala Ile Arg
 325 330 335
 Gly Asp Leu Val Val Ser Pro Ser Asp Asn Phe Phe Trp Phe His Arg
 340 345 350
 Pro Lys Leu Val Leu Leu Leu Ile His Ile Val Leu Phe Gln Asn Ala
 355 360 365
 Phe Glu Ile Ala Phe Phe Phe Trp Leu Leu Val Thr Tyr Gly Phe Lys
 370 375 380
 Ser Cys Ile Met Gly Lys Pro Ala Tyr Val Ile Thr Arg Val Val Ile
 385 390 395 400
 Ser Val Ile Cys Gln Val Leu Cys Gly Tyr Ser Thr Leu Pro Leu Tyr
 405 410 415
 Ala Val Val Ser His Met Gly Asn Ser Phe Lys Lys Thr Ile Phe Asp
 420 425 430
 Glu Asn Val Thr Glu Gly Leu Val Asn Trp Ala Glu Lys Ala Arg Arg
 435 440 445
 Gly Thr Arg Thr Pro Asn Lys Ile Thr Thr Asp Ala Ser Ser Ser Pro
 450 455 460
 Ile Asp Glu Ala Asn Gly Gly Ala Val Gln Met Thr Asn Thr Arg Ala
 465 470 475 480
 Asn Ser Ser Val Glu Gln Gly Thr Ala Arg Leu Ile
 485 490

<210> 39
 <211> 533
 <212> PRT
 <213> Hordeum vulgare

<400> 39
 Met Ser Asp Lys Lys Gly Val Pro Ala Arg Glu Leu Pro Glu Thr Pro
 1 5 10 15
 Ser Trp Ala Val Ala Val Val Phe Ala Ala Met Val Leu Val Ser Val
 20 25 30

Leu	Met	Glu	His	Gly	Leu	His	Lys	Leu	Gly	His	Trp	Phe	Gln	His	Arg		
		35					40					45					
His	Lys	Lys	Ala	Leu	Trp	Glu	Ala	Leu	Glu	Lys	Met	Lys	Ala	Glu	Leu		
	50					55					60						
Met	Leu	Val	Gly	Phe	Ile	Ser	Leu	Leu	Leu	Ile	Val	Thr	Gln	Asp	Pro		
65					70					75					80		
Ile	Ile	Ala	Lys	Ile	Cys	Ile	Ser	Glu	Asp	Ala	Ala	Asp	Val	Met	Trp		
				85					90					95			
Pro	Cys	Lys	Arg	Gly	Thr	Glu	Gly	Arg	Lys	Pro	Ser	Lys	Tyr	Val	Asp		
			100					105					110				
Tyr	Cys	Pro	Glu	Gly	Lys	Val	Ala	Leu	Met	Ser	Thr	Gly	Ser	Leu	His		
		115					120					125					
Gln	Leu	His	Val	Phe	Ile	Phe	Val	Leu	Ala	Val	Phe	His	Val	Thr	Tyr		
	130					135					140						
Ser	Val	Ile	Thr	Ile	Ala	Leu	Ser	Arg	Leu	Lys	Met	Arg	Thr	Trp	Lys		
145					150					155					160		
Lys	Trp	Glu	Thr	Glu	Thr	Thr	Ser	Leu	Glu	Tyr	Gln	Phe	Ala	Asn	Asp		
				165					170						175		
Pro	Ala	Arg	Phe	Arg	Phe	Thr	His	Gln	Thr	Ser	Phe	Val	Lys	Arg	His		
			180					185					190				
Leu	Gly	Leu	Ser	Ser	Thr	Pro	Gly	Ile	Arg	Trp	Val	Val	Ala	Phe	Phe		
		195					200					205					
Arg	Gln	Phe	Phe	Arg	Ser	Val	Thr	Lys	Val	Asp	Tyr	Leu	Thr	Leu	Arg		
	210					215					220						
Ala	Gly	Phe	Ile	Asn	Ala	His	Leu	Ser	Gln	Asn	Ser	Lys	Phe	Asp	Phe		
225					230					235					240		
His	Lys	Tyr	Ile	Lys	Arg	Ser	Met	Glu	Asp	Asp	Phe	Lys	Val	Val	Val		
				245					250					255			
Gly	Ile	Ser	Leu	Pro	Leu	Trp	Gly	Val	Ala	Ile	Leu	Thr	Leu	Phe	Leu		
			260					265					270				
Asp	Ile	Asn	Gly	Val	Gly	Thr	Leu	Ile	Trp	Ile	Ser	Phe	Ile	Pro	Leu		
	275						280					285					
Val	Ile	Leu	Leu	Cys	Val	Gly	Thr	Lys	Leu	Glu	Met	Ile	Ile	Met	Glu		
	290					295					300						
Met	Ala	Leu	Glu	Ile	Gln	Asp	Arg	Ala	Ser	Val	Ile	Lys	Gly	Ala	Pro		
305					310					315					320		
Val	Val	Glu	Pro	Ser	Asn	Lys	Phe	Phe	Trp	Phe	His	Arg	Pro	Asp	Trp		
				325					330					335			
Val	Leu	Phe	Phe	Ile	His	Leu	Thr	Leu	Phe	Gln	Asn	Ala	Phe	Gln	Met		
			340					345					350				

Ala His Phe Val Trp Thr Val Ala Thr Pro Gly Leu Lys Lys Cys Tyr
 355 360 365

His Thr Gln Ile Gly Leu Ser Ile Met Lys Val Val Val Gly Leu Ala
 370 375 380

Leu Gln Phe Leu Cys Ser Tyr Met Thr Phe Pro Leu Tyr Ala Leu Val
 385 390 395 400

Thr Gln Met Gly Ser Asn Met Lys Arg Ser Ile Phe Asp Glu Gln Thr
 405 410 415

Ser Lys Ala Leu Thr Asn Trp Arg Asn Thr Ala Lys Glu Lys Lys Lys
 420 425 430

Val Arg Asp Thr Asp Met Leu Met Ala Gln Met Ile Gly Asp Ala Thr
 435 440 445

Pro Ser Arg Gly Ser Ser Pro Met Pro Ser Arg Gly Ser Ser Pro Val
 450 455 460

His Leu Leu His Lys Gly Met Gly Arg Ser Asp Asp Pro Gln Ser Ala
 465 470 475 480

Pro Thr Ser Pro Arg Thr Gln Gln Glu Ala Arg Asp Met Tyr Pro Val
 485 490 495

Val Val Ala His Pro Val His Arg Leu Asn Pro Asn Asp Arg Arg Arg
 500 505 510

Ser Ala Ser Ser Ser Ala Leu Glu Ala Asp Ile Pro Ser Ala Asp Phe
 515 520 525

Ser Phe Ser Gln Gly
 530

<210> 40
 <211> 542
 <212> PRT
 <213> Arabidopsis thaliana

<400> 40
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Phe His Gly Gly Ala Thr Ala Thr Gly Ala Pro Ser Gly Gly Lys Glu
 20 25 30

Leu Ser Gln Thr Pro Thr Trp Ala Val Ala Val Val Cys Thr Phe Leu
 35 40 45

Ile Leu Ile Ser His Leu Leu Glu Lys Gly Leu Gln Arg Leu Ala Asn
 50 55 60

Trp Leu Trp Lys Lys His Lys Asn Ser Leu Leu Glu Ala Leu Glu Lys
 65 70 75 80

Ile Lys Ala Glu Leu Met Ile Leu Gly Phe Ile Ser Leu Leu Leu Thr
 85 90 95

Phe	Gly	Glu	Pro	Tyr	Ile	Leu	Lys	Ile	Cys	Val	Pro	Arg	Lys	Ala	Ala		
			100					105					110				
Leu	Ser	Met	Leu	Pro	Cys	Leu	Ser	Glu	Asp	Thr	Val	Leu	Phe	Gln	Lys		
		115					120					125					
Leu	Ala	Pro	Ser	Ser	Leu	Ser	Arg	His	Leu	Leu	Ala	Ala	Gly	Asp	Thr		
	130					135					140						
Ser	Ile	Asn	Cys	Lys	Gln	Gly	Ser	Glu	Pro	Leu	Ile	Thr	Leu	Lys	Gly		
145					150					155					160		
Leu	His	Gln	Leu	His	Ile	Leu	Leu	Phe	Phe	Leu	Ala	Ile	Phe	His	Ile		
				165					170					175			
Val	Tyr	Ser	Leu	Ile	Thr	Met	Met	Leu	Ser	Arg	Leu	Lys	Ile	Arg	Gly		
			180					185					190				
Trp	Lys	Lys	Trp	Glu	Gln	Glu	Thr	Leu	Ser	Asn	Asp	Tyr	Glu	Phe	Ser		
		195					200					205					
Ile	Asp	His	Ser	Arg	Leu	Arg	Leu	Thr	His	Glu	Thr	Ser	Phe	Val	Arg		
	210					215					220						
Glu	His	Thr	Ser	Phe	Trp	Thr	Thr	Thr	Pro	Phe	Phe	Phe	Tyr	Val	Gly		
225					230					235					240		
Cys	Phe	Phe	Arg	Gln	Phe	Phe	Val	Ser	Val	Glu	Arg	Thr	Asp	Tyr	Leu		
				245					250					255			
Thr	Leu	Arg	His	Gly	Phe	Ile	Ser	Ala	His	Leu	Ala	Pro	Gly	Arg	Lys		
			260					265					270				
Phe	Asn	Phe	Gln	Arg	Tyr	Ile	Lys	Arg	Ser	Leu	Glu	Asp	Asp	Phe	Lys		
		275					280					285					
Leu	Val	Val	Gly	Ile	Ser	Pro	Val	Leu	Trp	Ala	Ser	Phe	Val	Ile	Phe		
	290					295					300						
Leu	Leu	Phe	Asn	Val	Asn	Gly	Trp	Arg	Thr	Leu	Phe	Trp	Ala	Ser	Ile		
305					310					315					320		
Pro	Pro	Leu	Leu	Ile	Ile	Leu	Ala	Val	Gly	Thr	Lys	Leu	Gln	Ala	Ile		
				325					330					335			
Met	Ala	Thr	Met	Ala	Leu	Glu	Ile	Val	Glu	Thr	His	Ala	Val	Val	Gln		
			340					345					350				
Gly	Met	Pro	Leu	Val	Gln	Gly	Ser	Asp	Arg	Tyr	Phe	Trp	Phe	Asp	Cys		
		355					360					365					
Pro	Gln	Leu	Leu	Leu	His	Leu	Ile	His	Phe	Ala	Leu	Phe	Gln	Asn	Ala		
						375						380					
Phe	Gln	Ile	Thr	His	Phe	Phe	Trp	Ile	Trp	Tyr	Ser	Phe	Gly	Leu	Lys		
385					390					395					400		
Ser	Cys	Phe	His	Lys	Asp	Phe	Asn	Leu	Val	Ser	Lys	Leu	Phe	Leu			
				405					410				415				

Cys Leu Gly Ala Leu Ile Leu Cys Ser Tyr Ile Thr Leu Pro Leu Tyr
 420 425 430
 Ala Leu Val Thr Gln Met Gly Ser His Met Lys Lys Ala Val Phe Asp
 435 440 445
 Glu Gln Met Ala Lys Ala Leu Lys Lys Trp His Lys Asp Ile Lys Leu
 450 455 460
 Lys Lys Gly Lys Ala Arg Lys Leu Pro Ser Lys Thr Leu Gly Val Ser
 465 470 475 480
 Glu Ser Phe Ser Leu Ser Ser Ser Ser Ser Ala Thr Thr Leu His Arg
 485 490 495
 Ser Lys Thr Thr Gly His Ser Ser Asn Ile Ile Tyr Tyr Lys Gln Glu
 500 505 510
 Asp Glu Glu Asp Glu Met Ser Asp Leu Glu Ala Gly Ala Glu Asp Ala
 515 520 525
 Ile Asp Arg Ile Gln Gln Gln Glu Met Gln Phe His Asn Ser
 530 535 540

<210> 41
 <211> 526
 <212> PRT
 <213> Arabidopsis thaliana

<400> 41
 Met Gly His Gly Gly Glu Gly Met Ser Leu Glu Phe Thr Pro Thr Trp
 1 5 10 15
 Val Val Ala Gly Val Cys Thr Val Ile Val Ala Ile Ser Leu Ala Val
 20 25 30
 Glu Arg Leu Leu His Tyr Phe Gly Thr Val Leu Lys Lys Lys Lys Gln
 35 40 45
 Lys Pro Leu Tyr Glu Ala Leu Gln Lys Val Lys Glu Glu Leu Met Leu
 50 55 60
 Leu Gly Phe Ile Ser Leu Leu Leu Thr Val Phe Gln Gly Leu Ile Ser
 65 70 75 80
 Lys Phe Cys Val Lys Glu Asn Val Leu Met His Met Leu Pro Cys Ser
 85 90 95
 Leu Asp Ser Arg Arg Glu Ala Gly Ala Ser Glu His Lys Asn Val Thr
 100 105 110
 Ala Lys Glu His Phe Gln Thr Phe Leu Pro Ile Val Gly Thr Thr Arg
 115 120 125
 Arg Leu Leu Ala Glu His Ala Ala Val Gln Val Gly Tyr Cys Ser Glu
 130 135 140
 Lys Gly Lys Val Pro Leu Leu Ser Leu Glu Ala Leu His His Leu His
 145 150 155 160

Ile	Phe	Ile	Phe	Val	Leu	Ala	Ile	Ser	His	Val	Thr	Phe	Cys	Val	Leu	165	170	175
Thr	Val	Ile	Phe	Gly	Ser	Thr	Arg	Ile	His	Gln	Trp	Lys	Lys	Trp	Glu	180	185	190
Asp	Ser	Ile	Ala	Asp	Glu	Lys	Phe	Asp	Pro	Glu	Thr	Ala	Leu	Arg	Lys	195	200	205
Arg	Arg	Val	Thr	His	Val	His	Asn	His	Ala	Phe	Ile	Lys	Glu	His	Phe	210	215	220
Leu	Gly	Ile	Gly	Lys	Asp	Ser	Val	Ile	Leu	Gly	Trp	Thr	Gln	Ser	Phe	225	230	235
Leu	Lys	Gln	Phe	Tyr	Asp	Ser	Val	Thr	Lys	Ser	Asp	Tyr	Val	Thr	Leu	245	250	255
Arg	Leu	Gly	Phe	Ile	Met	Thr	His	Cys	Lys	Gly	Asn	Pro	Lys	Leu	Asn	260	265	270
Phe	His	Lys	Tyr	Met	Met	Arg	Ala	Leu	Glu	Asp	Asp	Phe	Lys	Gln	Val	275	280	285
Val	Gly	Ile	Ser	Trp	Tyr	Leu	Trp	Ile	Phe	Val	Val	Ile	Phe	Leu	Leu	290	295	300
Leu	Asn	Val	Asn	Gly	Trp	His	Thr	Tyr	Phe	Trp	Ile	Ala	Phe	Ile	Pro	305	310	315
Phe	Ala	Leu	Leu	Leu	Ala	Val	Gly	Thr	Lys	Leu	Glu	His	Val	Ile	Ala	325	330	335
Gln	Leu	Ala	His	Glu	Val	Ala	Glu	Lys	His	Val	Ala	Ile	Glu	Gly	Asp	340	345	350
Leu	Val	Val	Lys	Pro	Ser	Asp	Glu	His	Phe	Trp	Phe	Ser	Lys	Pro	Gln	355	360	365
Ile	Val	Leu	Tyr	Leu	Ile	His	Phe	Ile	Leu	Phe	Gln	Asn	Ala	Phe	Glu	370	375	380
Ile	Ala	Phe	Phe	Phe	Trp	Ile	Trp	Val	Thr	Tyr	Gly	Phe	Asp	Ser	Cys	385	390	395
Ile	Met	Gly	Gln	Val	Arg	Tyr	Ile	Val	Pro	Arg	Leu	Val	Ile	Gly	Val	405	410	415
Phe	Ile	Gln	Val	Leu	Cys	Ser	Tyr	Ser	Thr	Leu	Pro	Leu	Tyr	Ala	Ile	420	425	430
Val	Ser	Gln	Met	Gly	Ser	Ser	Phe	Lys	Lys	Ala	Ile	Phe	Glu	Glu	Asn	435	440	445
Val	Gln	Val	Gly	Leu	Val	Gly	Trp	Ala	Gln	Lys	Val	Lys	Gln	Lys	Arg	450	455	460
Asp	Leu	Lys	Ala	Ala	Ala	Ser	Asn	Gly	Asp	Glu	Gly	Ser	Ser	Gln	Ala	465	470	475

Gly Pro Gly Pro Asp Ser Gly Ser Gly Ser Ala Pro Ala Ala Gly Pro
485 490 495

Gly Ala Gly Phe Ala Gly Ile Gln Leu Ser Arg Val Thr Arg Asn Asn
500 505 510

Ala Gly Asp Thr Asn Asn Glu Ile Thr Pro Asp His Asn Asn
515 520 525

<210> 42

<211> 583

<212> PRT

<213> Arabidopsis thaliana

<400> 42

Met Ala Asp Gln Val Lys Glu Lys Thr Leu Glu Glu Thr Ser Thr Trp
1 5 10 15

Ala Val Ala Val Val Cys Phe Val Leu Leu Leu Ile Ser Ile Val Ile
20 25 30

Glu Lys Leu Ile His Lys Ile Gly Ser Trp Phe Lys Lys Lys Asn Lys
35 40 45

Lys Ala Leu Tyr Glu Ala Leu Glu Lys Val Lys Ala Glu Leu Met Leu
50 55 60

Met Gly Phe Ile Ser Leu Leu Leu Thr Ile Gly Gln Gly Tyr Ile Ser
65 70 75 80

Asn Ile Cys Ile Pro Lys Asn Ile Ala Ala Ser Met His Pro Cys Ser
85 90 95

Ala Ser Glu Glu Ala Arg Lys Tyr Gly Lys Lys Asp Val Pro Lys Glu
100 105 110

Asp Glu Glu Glu Asn Leu Arg Arg Lys Leu Leu Gln Leu Val Asp Ser
115 120 125

Leu Ile Pro Arg Arg Ser Leu Ala Thr Lys Gly Tyr Asp Lys Cys Ala
130 135 140

Glu Lys Gly Lys Val Ala Phe Val Ser Ala Tyr Gly Met His Gln Leu
145 150 155 160

His Ile Phe Ile Phe Val Leu Ala Val Cys His Val Ile Tyr Cys Ile
165 170 175

Val Thr Tyr Ala Leu Gly Lys Thr Lys Met Arg Arg Trp Lys Lys Trp
180 185 190

Glu Glu Glu Thr Lys Thr Ile Glu Tyr Gln Tyr Ser His Asp Pro Glu
195 200 205

Arg Phe Arg Phe Ala Arg Asp Thr Ser Phe Gly Arg Arg His Leu Ser
210 215 220

Phe Trp Ser Lys Ser Thr Ile Thr Leu Trp Ile Val Cys Phe Phe Arg
225 230 235 240

Gln	Phe	Phe	Arg	Ser	Val	Thr	Lys	Val	Asp	Tyr	Leu	Thr	Leu	Arg	His	245	250	255	
Gly	Phe	Ile	Met	Ala	His	Leu	Ala	Pro	Gly	Ser	Asp	Ala	Arg	Phe	Asp	260	265	270	
Phe	Arg	Lys	Tyr	Ile	Gln	Arg	Ser	Leu	Glu	Glu	Asp	Phe	Lys	Thr	Ile	275	280	285	
Val	Glu	Ile	Asn	Pro	Val	Ile	Trp	Phe	Ile	Ala	Val	Leu	Phe	Leu	Leu	290	295	300	
Thr	Asn	Thr	Asn	Gly	Leu	Asn	Ser	Tyr	Leu	Trp	Leu	Pro	Phe	Ile	Pro	305	310	315	320
Phe	Ile	Val	Ile	Leu	Ile	Val	Gly	Thr	Lys	Leu	Gln	Val	Ile	Ile	Thr	325	330	335	
Lys	Leu	Gly	Leu	Arg	Ile	Gln	Glu	Lys	Gly	Asp	Val	Val	Lys	Gly	Thr	340	345	350	
Pro	Leu	Val	Gln	Pro	Gly	Asp	His	Phe	Phe	Trp	Phe	Gly	Arg	Pro	Arg	355	360	365	
Phe	Ile	Leu	Phe	Leu	Ile	His	Leu	Val	Leu	Phe	Thr	Asn	Ala	Phe	Gln	370	375	380	
Leu	Ala	Phe	Phe	Val	Trp	Ser	Thr	Tyr	Glu	Phe	Gly	Leu	Lys	Asn	Cys	385	390	395	400
Phe	His	Glu	Ser	Arg	Val	Asp	Val	Ile	Ile	Arg	Ile	Ser	Ile	Gly	Leu	405	410	415	
Leu	Val	Gln	Ile	Leu	Cys	Ser	Tyr	Val	Thr	Leu	Pro	Leu	Tyr	Ala	Leu	420	425	430	
Val	Thr	Gln	Met	Gly	Ser	Lys	Met	Lys	Pro	Thr	Val	Phe	Asn	Glu	Arg	435	440	445	
Val	Ala	Thr	Ala	Leu	Lys	Ser	Trp	His	His	Thr	Ala	Lys	Lys	Asn	Ile	450	455	460	
Lys	His	Gly	Arg	Thr	Ser	Glu	Ser	Thr	Thr	Pro	Phe	Ser	Ser	Arg	Pro	465	470	475	480
Thr	Thr	Pro	Thr	His	Gly	Ser	Ser	Pro	Ile	His	Leu	Leu	Arg	Asn	Ala	485	490	495	
Pro	His	Lys	Arg	Ser	Arg	Ser	Val	Asp	Glu	Ser	Phe	Ala	Asn	Ser	Phe	500	505	510	
Ser	Pro	Arg	Asn	Ser	Asp	Phe	Asp	Ser	Trp	Asp	Pro	Glu	Ser	Gln	His	515	520	525	
Glu	Thr	Ala	Glu	Thr	Ser	Asn	Ser	Asn	His	Arg	Ser	Arg	Phe	Gly	Glu	530	535	540	
Glu	Glu	Ser	Glu	Lys	Lys	Phe	Val	Ser	Ser	Ser	Val	Glu	Leu	Pro	Pro	545	550	555	560

Gly Pro Gly Gln Ile Arg Thr Gln His Glu Ile Ser Thr Ile Ser Leu
565 570 575

Arg Asp Phe Ser Phe Lys Arg
580